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Command line parameters:

-MODEL-frame+_n2p.model -DEV=x1p
-Q-/cgn2_1/USPTO_spool/VIS09965830/runat_07052003_151448_6247/app_que
-DB=Swissprot_40 -QFMM-fastan -SUFFIX=rsp -MINMATCH=0.1 -LOOPCL=0 -L
-DN-TIS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANG-human40.cdi -LI
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE
-MOCALIGN=200 -MAN=ext -HeAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09965830_@CGN_1_1_70_@runat_07052003_151448_6247 -NCPU=6 -USER-US09965830_@CGN_1_1_70_@runat_07052003_151448_6247 -NCPU=6 -NANN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPF
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , )
Ygapop 10.0 , )
Fgapop 6.0 , F
Delop 6.0 , I
              SwissProt_40:*
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tion	RL Proc. Natl. Acad. Sci. U.S.A. 91:3438-3442(1994)
nomo sapien	
os taurus ',	Itoh T., Tanaka T., Nagai R., Kamiya T., Sawayama T
cgmp-gate	An Juliotke H., Sakurada H., Yazaki Y., Nakamura Y.,
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"Novel missense mutation
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Haneda N., Nakano O., Shibata
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Satler C.A., Vesely M.R., Duggal P., Ginsburg "Multiple different missense mutations in the patients with long QT syndrome.";
Hum. Genet. 102:265-272(1998).
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                                                                                                                                                                                                                                         "Novel missense mutation syndrome family.";
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                                                               "High-throughput single-strand conformation polymorphism analys automated capillary electrophoresis: robust multiplex analysis pattern-based identification of allelic variants.";
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                      VARIANTS LQT2 L-29
MEDLINE-99214568;
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Momma K., Matsuoka R.;
 syndrome-associated
           Zou A.,
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h E.P., Vesely M
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               Splawski
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                        9; T-33; R-53; Q-56; PubMed=10187793;
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Sawayama T., Kasai H., Yazaki Y.,
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                                                                                                                                                            Dutch long-QT families.";
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               Sanguinetti M.C.;
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MEDLINE=99445248; PubMed=10517660; Yoshida H., Horie M., Otani H., Ta Fukunami M., Sasayama S.;
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J. Biol. Chem. 274:10113-10118(1999).
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Splawski I., Shen J., Timothy K.W., Lehmann M.H., Priori
Robinson J.L., Moss A.J., Schwartz P.J., Towbin J.A., Vir
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Moller M., Sorensen
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. cardiovasc. Electrophysiol. 10:1262-1270(199
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OF THE INWARD-RECTIFYING POTASSIUM CHANNELS.

SIMILARITY: CONTAINS 1 CYCLIC NUCLECTIBE-BINDLING DOMAIN. SIMILARITY: CONTAINS 1 PAS (PER-ARMY-SIM) DIMERIZATION DIMINIARITY: CONTAINS 1 PAS -ASSOCIATED C-TERMINAL (PAC) DIMERIZATION D
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART.

DISEASE: DEFECTS IN KOH12 ARE ASSOCIATED WITH LONG QT SYNDROME
DISEASE: DEFECTS IN KOH12 ARE ASSOCIATED WITH LONG QT SYNDROME
TYPE 2 (LQT2). THIS DISEASE IS CHARACTERIZED BY A PROLONGED QT
TYPE 2 (LQT2). THIS DISEASE IS CHARACTERIZED BY A RRHYTHMIAS KNOWN
BEGMENT ON THE ECG AND DAYMORPHIC VENTREIN IN CECURENT IN RELATION
AS TORSADES DE POINTES. THESE ARRHYTHMIAS OFFEN IN RECURRENT
TO EXERCISE OR EMOTIONAL STRESS AND MAY RESULT IN RECURRENT
TO EXERCISE OR EMOTIONAL STRESS AND MAY RESULT IN RECURRENT
SYNCOPE. SEIZURES, OR SUDDEN CARDIAC DEATH. DEAFNESS IS OFTEN

SYNCOPE. SEIZURES, OR SUDDEN CARDIAC DEATH. DEAFNESS IS OFTEN
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                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                         equires a license agreement (See http://www.isb-sib.chemail to license@isb-sib.ch).
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Svendsen I.H., Jensen
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	1980	1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCCGGCGGGAGCAGGTGGTAAAGGCCAATGCC	QΥ
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	760	741 LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr	Вb
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	740	721 ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys	망
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	o UT	04 GCCATCATCCAGCGCATGTACGCCCGCGCGCTTTCTGTACCACGCGCGCACGCGGCGCGCCCTTTCTGTACCACGAGCCGCGCGCG	QY
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	1503	ATCGGCGCCCTGATGCACGCGGTGGTGTTTGGGAACGTGAC	Qy
	640	621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe	Ъ
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01-JUL-1993 (Rel. 26, Created)

01-JUL-1993 (Rel. 26, Last seq

16-OCT-2001 (Rel. 40, Last ann
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16-OCT-2001 (Rel. 40, Last annotation updat
Potassium channel protein eag.
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
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                                                                                                                                                                                                                                                                                                                                                                           Ionic channel;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (sor send an email to license@isb-sib.ch).
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InterPro; IPR000636; M+channel_nlg.
InterPro; IPR001610; pAC.
InterPro; IPR000700; PAS-assoc_C.
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MEDLINE-91262635; PubMed=1840699,
Warmke J., Drysdale R., Ganetzky
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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27; SM00086; PAC; 1.
27; SM00091; PAS; 1.
27; SM00100; CNMP; 1.
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SIMILARITY: CONTAINS 1 CYCLIC NUCLEOTIDE-BINDING DOMAIN.
SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
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SUBCELLULAR LOCATION: Integ
MISCELLANEOUS: THE SEGMENT
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228 79

GCCTGCACGACAGCCTTGCGCTGTACCCC 2058	99 TACTGCGTCCTGCAGTGTCTGCAGCTGGCTGGCCTGC	Qy 19
AsnValArgAl	36 AspGlnPheTrpLysAspSerAlaVal	6
GACGTGAAGGG	39 TGTGAGCTGCCCCGGCGGGAGCAGGTGG	Qy 19:
ACCGTGCTCGCCATCCTAGGGAAGGGCGACCTGATCGGC 1938 ::: ::: GluValValAlaIleLeuGlyLySGlyAspValPheGly 635	79 ATGGAGGTGCTCAAGGGTGGC:::: ::::::	Qy 187 рь 63
GCTCC 18	19 GAGTACCTCATCCACCAAGGC ::: 96 AspLeuLeuTyrHisThrGly	Qy 181 Db 59
GGCCCTGCGGCCCGCCTTCTGCACGCCGGGC 1818 : tHisPheMetMetSerHisSerAlaProGly 595	59 AGCCGCGGCTGCCTGCGGGCACTGTCTCT	Qy .175 Db 57
GCCACTGTT: sProThrPhe	02 GACATCGCCATGCACCTGCACAAGGAGGTV 	Qy 170
TGCAGAGCCTCCCTGACGAGCTGCGCGCA 1701 :::::::	42 GTGAACAATGGCATCGACACCACCGAGCTGCTGCAGAG ::: ::: 36 MetThrLysGlyLeuAspThrGluLysValLeuAsnCy	Qy 164 Db 53
TGCTGGAGTACTTCCAGGCCACCTCGGCC 1641 :::::: 	82 CACCGTATCCCCAAGCCCCTCAAGCAGCGCATGCTC	5 15
CGCGCGACCTGCGCGACTACATCCGCATC 1581 ::::: :::::::::::::::::::::::::::::	22 TACGCCCGCCGCTTTCTGTACCACAGCCGCACGCGCGACCTGCGC :::::: 96 ThrSerAlaThrAlaLysTyrHisAspMetLeuasnAsnValArg	Qy 152 Db 49
CCAGCGCATG 1 ::: eGlnGlnMet 4	62 ATCGGCGCCCTGATGCACGCGGTGGTGTTTGGGAACGTGACGGCCATCAT	14
GCCAACACGGACACCGAGAAGATCTTCTCCATCTGCACCATGCTC 1461	2 TTCGGCAACGTGTCC	14
rcgcacrcagcagccrcaccagccrgggc 1401 ::::: ::: heThrMetThrCysMetThrSerValG1y 455	2 CTGCGCAGCGCCTAC ::: 6 ArgLysSerMetTyr	Qy 134 Db 43
:GCTGGAGCTGCTGGGC ::: yProGluLeuValAsn	AACTGCAGCAGCAGCAGCGAGGCCAACGGGACG	Qy 128 Db 42
GAACAGCTCCGGCC	ACTCCCTACTACCTGGTGGGCCGGAGGCCAGCTGGAGGG::: SerProTyrSerTyr1leTrp	Qy 1222 Db 416
GGAGCTGGCCGCCGACTGGAG 1 ::: pLysLeuAlaAsnValThrGln 4	2 AGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGC ::: 0 AsnGly	Qy 116 рь 40
GTTTTACATTGGCCAGCGGGAGATCGAG 1161 -:: :: :: :: PTyrSerIleGlyArgSerAspAlaAsp 399	2 GCCTGCTCGCGCACTGGGTCGCCTGCGTCTGTTTT	Qy 110 Db 38
AGCGCCGTGGTGCTGACACTGCTCATGGCCGTGTTC 1101 :: ::: 379	2 CGGCTGGACCGGTACTCGCAGTAC ::: 0 LysLeuAspArgTyrLeuGluTyr	Qy 104: Db 36
CCTGCTGCGCCTGCTGCGCCTGCTTCCG 1041	32 TACTTCGGGGCCCATCTGCTGAAGACGGTGCGCCTGCTGCGCCCTGCTGCGCCCTGCTGCGCCCTGCTG	Qy 98: Db 34:
AAGGTCAACG ::: AspargaspGluaspGlyIleGlyS	7 GCAGCGCTGCCCT ::: : 2 SerCysLeuProT	Qy 93.

Qy

282	2826	Qy	
982	963 GlyThrProThrThrGlnAlaProProThrSerAlaValThrSerProValAspThrVal	.∵ Dp	٠,٠
282	2818	, Qy	
,	ysGlyAlaGlyGlyGl	₽	
942	GlyGluL	Db	
2790	2731 GCGCCCACAGGGAGGGTCCGTGCCCTGGGCATCGGGAGAGGGGCCGTGCCCAGGCAGCC	Qy	
N	903 AspValArgLeuGluLeuGlnArgMetGlnGlnArgIleGl	Db 43	
2730	FROM THE PROPROTITION THE PARTIES OF THE PARTIES OF THE PROPROTITION OF THE PROPROTITION OF THE PARTIES OF THE	O D	
2685	47	Qy	
2646 882	2593GTTCCCCATGGGCCCAGCGAGGCAAGGAACACAGACACTGGACAAG;CTTCGG 	Qγ	
862	::::: 843 GlyThrValValAlaIleValThrLysAlaAspArgAsnLeuAlaLeuGluArgGluArg	В	
2592	2584	Qy	
2583 842	2545 GAATGTAGCAGCAGCCCCTCCCCTGGACCAGAGAGCGGC :::::: :::::: 823 ValAlaThrThrSerSerAlaAlaGlyAlaGlyValSerGlyGlyProGlySerGly	Qу	
2544 822	2485 GAAGACGGCTGTGGCTCGGACCAGCCCAAGTTCTCTTTCCGCGTGGGCCAGTCTGGCCCGG	Фу	
2484 807	2443AATGTGCCCCCAGATCTGAGCCCCAGGGTAGTAGATGGCATT :::	Ф	
789	 ProLysAlaProLysLeuGlnAlaSerGlnAlaThrLeuAlaArgGlnAspThrIleAsp	•	
4	CCTTTGCTCCCCACGGGCCCTAGAGGGGCTACGGCTGCCCCCCATGCCATGG	Q 5	
2388 769	2359 AGGCCAGGGGCTTTGAAGGCTGAGGCTGGC		
2358 749	2299 CTGCTATCCCCACGTCGAACAGCACCCCGGCCTCGTCTAGGTGGCAGAGGGAGG	Фу	
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2238 714	2179 ACGCTGGAGGAGAAGGAGACAGATGGGGAGGAGGGCCCCACGGTCTCCCCCAGCCCCAGCCT :	рь ф у	
694	692ArgHisArg (Db	
2178	2119 GGGGGAGGCTCTGCAGAGGTGGACACCAGCTCCCTGAGCGGCGACAATACCCTTATGTCC ;	Qy 	
691			
675 2118	P. P.	0 pb	

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FAMILY

SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: TESTIS, KIDNEY, RETINAL CONE, A
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED

AND

AND HEART.
CATION CHANNEL

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                       "Another member of the Circular and heart."; expressed in testis, kidney, and heart."; Proc. Natl. Acad. Sci. U.S.A. 91:3505-3509(1994).
-!- FUNCTION: COULD BE RESPONSIBLE FOR CGMP-INDUCED CALCIUM ENTRY IN CENSCRY CELLS. MIGHT BE INVOLVED IN CHEMOTAXIS (
                                                                                                                                                                                                                   TISUE=Testis;
MEDLINE=94211295; PubMed=7512693;
Wavand I., Godde M., Frings S., Weiner
                                                                              MEDLINE-94224768; PubMed-8170936;
Biel M., Zong X., Distler M., Bosse E., Klugbauer N., Melockerzi V., Hofmann F.;
Another member of the cyclic nucleotide gated channel
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                                                                                                                                                                                                                                                                                                                                                                      Cyclic-nucleotide-gated cation channel alpha 3 (CNG-3) (CNG3) (Cyclic nucleotide gated channel photoreceptor cGMP-gated channel alpha subunit).
                                                                                                                                                                                            "Cloning and functional expression of channel from mammalian sperm.";
                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, last annotation
                                                                                                                                             TISSUE=Kidney;
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                 Nature 368:859-863(1994).
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SUBUNIT: FORMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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        FUNCTIONAL
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Lalpha 3) (Cone
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TRANSMEM 186
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                                                                                                                                                                                                                                                                           141
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PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE; PS50042; CNMP_BINDING_3; 1.
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InterPro; IPR000595; cNMP_binding.
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GCCGTGGAGGTCCTCTTCATCCTTGACATTGTGCTGAATTTCCGTACCACATTCGTGTCC
                       \hbox{\tt ---AlaCysPheAspGluLeuGlnSerGluHisLeuMetLeuTrpLeuValLeuAspTyr}
                                                                                              TrpLeuThrVal
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                                                                                                                                                                                                                                            CAGAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGGGTGTTTTGGGGAGAAACCAAAC
                                                                        ValPheTyrAsnTrpCysLeuLeuValCysArg---
                                                                                                                                             GCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTCACT
                                                                                                                                                                     LysGluGluLysLysLysAspSerValValMetAspProSerSerAsnMetTyrTyrHis
                                                                                                                                                                                                                                                                                          GGCTTCAATGCCAACCGGCGGCGGAGCCGGGCCGTGCTCTACCACCTGTCCGGGCACCTG
                                                                                                                                                                                             TTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGTGGG
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EMBL; U48803; AAA92110.1; EMBL; U93851; AAC53139.1; EMBL; U76220; AAC17594.1;

IPR000636;

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CNGA1 OR CNCG1 OR CNCG.
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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Barnstable C.J., Wei J.Y
Submitted (MAR-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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J. Neurosci. 17:1993-2005(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ding C., Potter E.D., Qiu W., Coon S. "Cloning and widespread distribution nucleotide-gated cation channel.";
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MEDLINE=97197878; PubMed=9045728;
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                                                                                                        use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                      PHOTORECEPTORS.
SUBUNIT: HOMOTETRAMER OR HIGHER OLIGOMER.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: ROD CELLS IN THE RETINA.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GAN
                                                                                                                                                                                                                                                                                               FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Physiol. 272:Cl335-Cl344(1997).
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                                                                                                                                        ween the Swiss Institute of Bioinformatics Institute.
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an email to license@isb-sib.ch)
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CNG3_HUMAN
WARLANTS RULL, AND CONTROL OF PUBMED-1862398;
MEDLINE-98324775; PubMed-9662398;
KOhl S., Marx T., Glddings I., Jaegle H., Jacobson S.G.,
Apfelstedt-Sylla E., Zrenner E., Sharpe L.T., Wissinger B.;
Apfelstedt-Sylla E., Zrenner E., Sharpe L.T., Wissinger B.;
"Total colourblindness is caused by mutations in the gene encoding."
"Total colourblindness is caused by mutations in the gene encoding."
                                                                                                                                                                                                             gene encoding the alpha-subunit cone photoreceptors.";
Eur. J. Neurosci. 9:2512-2521(19)
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Cyclic-nucleotide-gated cation channel alpha 3 (CNG ch
(CNG-3) (CNG3) (Cyclic nucleotide gated channel alpha
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CNGA3 OR CNCG3.
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                                                                                                                                                                                                                                            chromosomal localization and ding the alpha-subunit of the
                                                                                                                          of cyclic nucleotide-gated cells.";
                                                                                                                                                                                    320-580 FROM N.A.
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FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY COUPLED CASCADE USING COMP AS SECOND MESSENGER. THIS BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING
                      DISEASE: DEFECTS IN CNGA3 ARE A CAUSE OF ROD MONOCHROMACY
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use by non-profit institutions as long a modified and this statement is not removed. entities between send s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its DATABASE: NAME=Mutations of the CNGA3 gene;
NOTE=Retina International's Scientific Newsletter;
WWWW="http://www.retina-international.com/sci-news/cnga3mut.htm" RM); ALSO KNOWN AS TOTAL COLORBLINDNESS OR ACHROMATOPSIA. AN AUTOSOMAL RECESSIVELY INHERITED CONDITION. SIMILARITY: an email to license@isb-sib.ch). requires a BELONGS TO THE CYCLIC ormatics Institute. There are no resi license agreement (See http://www.isb-sib.ch/announce/ NUCLEOTIDE-GATED CATION CHANNEL Usage by and for commercial 1n

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Pfam; PF00027; cNMP_binding; 1. Pfam; PF00520; ion_trans; 1. SMART; SM00100; CNMP; 1. TRANSMEM TRANSMEM EMBL; AF065314; AAC17440.1; EMBL; S76069; AAD14208 1 NP_BIND MIM; 216900; SEQUENCE VARIANI VARIANI VARIANI VARIANT VARIANI VARIANI VARIANT BINDING TRANSMEM Multigene PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE; PS50042; CNMP_BINDING_3; 1. PROSITE; PS00888; CNMP_BINDING_1; 1. InterPro; IPR001622; InterPro; IPR000636; InterPro; IPR000595; VARIANT VARIANI Ionic channel; Scores: HGNC:2150; CNGA3 694 171 305 378 482 549 564 557 547 529 410 283 283 163 ă, Ion Vision; 557 547 529 410 291 283 283 163 4.84e-10 78838 MW; K+channel_pore.
M+channel_nlg. cNMP_binding Disease mutation; Polymorphism CAMP CAMP /FTId=VAR_010910 V -> M (IN RMCH) /FTId=VAR_010907 /FTId=VAR_010903 R -> Q (IN RMCH) POTENTIAL POTENTIAL POTENTIAL /FTId=VAR_010906 /FTId=VAR_010905 T -> R (IN RMCH) /FTId=VAR_010902 cAMP-binding; Transmembrane; /FTId=VAR_010908 /FTId=VAR ţ ÿ AE00B4EE760D70A0 -> L (IN RMCH) W (IN RMCH) W (IN RMCH) L (IN R (IN RMCH) (POTENTIAL) (POTENTIAL) _010904 CRC64; 694 142 95 217 107

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	411	392 PheAlaThrIleValGlyAsnValGlySerMetIleSerAsnMetAsnAlaSerArgAla	DЬ
	1536	STGTTTGGG	Qy
	391	372 ProValLysAspGluGluTyrLeuPheValValValAspPheLeuValGlyValLeuIle	В
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	1236	GCCTGAGATTGGCTGGCTGCAGGAGCTGGCCCGCCGACTGGAGACTCCCTACTACC	Qy
	326	TrpAsnAlaCysIleTyrPh	
	1176	GCCTGCGTCTGGTTTTACATTGGCCAGCGGGAGATCGAGAGCAGCGAATC	Qy
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Boenigk W., Altenhofen W., Mueller F., Dose A., Illing M.,
Molday R.S., Kaupp U.B.;
"Rod and cone photoreceptor cells express distinct genes for
CGMP-gated channels.";
Neuron 10:865-877(1993).
-1- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN
COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN
BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION
CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF CONE
                                                                                                                                                                                                                                                                                                                                                                                                                         CNG1_CHICK
Q90805;
01-NOV-1997
                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=93264082; PubMed=7684234;
                                                                                                                                                                                                                                                                   Gallus.
                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken)
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cyclic nucleotice gated channel, cone photoreceptor, alpha subunit (CNG channel) (CNG-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2383 GCT 2385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasiani
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                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00888; CNMP_BINDING_1; 1. PROSITE; PS00889; CNMP_BINDING_2; 1. PROSITE; PS50042; CNMP_BINDING_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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InterPro; IPR000595; cNMP_binding.
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144 eSerAsnAsnThrAsnGluAspLysLysGluGluLysLysGluValLysGluGluLysLy 164
                                                                                                                      107 GluLeuvalGluValSerSerArgGlnSerAsnIleArgSerPheLeuGlyIleArgGlu 126
                                                                                                                                                                                   87
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
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                                                          GlnProGlyGlyValAsnGlyProTrpPro-----LeuAlaArg-PheAsnValAsnPh 144
                                                                                        TGGCCGGCGCCGATA-----TGGCCGGGCACGATCCAAAGGCTTCAATGCCAAC-- 498
                                                                                                                                                     CGACAGATGGAA----
                                                                                                                                                                                   ArgHisLeuHisHisGluAspGlnArgProAspSerPheLeuGluArgIleArgGlyPro 106
                                                                                                                                                                                                                -----CATCAGCGAAACCAAGAACCG-----
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H1 (POTENTIAL).
                             -CGGCGGCGGAGCCGGGCCGTGCTCTACCACCTGTC 533
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Matches:
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1461 CATCGGCGCCTGATGCACGCGGTGGTGTTTGGGAACGTGACGGCCATCATCCAGCGCAT	1401 CTTCGGCAACGTGTCCGCCAACACGGACACCGAGAGATCTTCTCCATCTGCACCTGCT	1341 GCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTCAGCAGCCTCACCAGCGTGGG	393	1281 CAACTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGGCTGGAGCTGCTGGGCGGCCCGTC	393	-	1174GAGCTGCCTGAGATTGGCTGGCTGGAGGAGCTGGCCCGCCGACTGGA :::	pAsnAlaCysIleTyrPheAlaIleSerLysValIleGlyPheGlyThrAspSerTrpVa	1119 GGTCGCCTGCGTCTGGTTTTACATTGGCCAGCGGAGATCGAGAGAGCAGCGAATCC	343 eArgileGlyAsnLeuValLeuTyrileLeu	eAlaArgueupheGluphePheAspargUnrGlurnrArgThrAshTyrroAshMetPh	GCTGCGCTTCCGCGCGGCTGGACCGGTACTCG		966 CTTCAAGGTCAACGTGTACTTCGGGGGCCCATCTGCTGAAGACGGTGCGCCTGCTGCTGCCCT	909 CACCACCTGGTTCCTGCTGGATGTCATCGCAGCGCTGCCTTTGACCTGCTACATGC	::: ::: ::: :::		793GAUCTIGGUGTIGGAGGTUCTUTTGATUTGTGTGTGAATTTUCGTGACACT 	uznandiinanskinatistudsvariitsnamingkaliiskonus (2000)	CGGCCCGCCCAGCGTCTGT	217 eAlaAlaProValPheTyrAsnTrpCYsMetLeuIleCysArg	GAGCCCAGTGCCGCCCG	204 pProSerSerAsnMetTyrTyrAsnTrpLeuThrIleI1	654 GCACTGTGGGGCACTGAGAGCCACCTGGGGATGGCTTCATCCTGCTCGCCACACTCTATGT	184 sAspAspLysLysAspAspLysLysGluGluGlnLysLysGluValPheValIleAs		534 CGGGCACCTGCAGAAGCCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGGTGTTTGGGGA :::::::::::::::::::	
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                       Biel M., Seeliger M., Pfelfer A., Kohler K., Gers Jaissle G., Fauser S., Zrenner E., Hofmann F.; "Selective loss of cone function in mice lacking nucleotide gated channel CNG3.", Proc. Natl. Acad. Sci. U.S.A. 96:7553-7557(1999).
                                                                                                                                                                                                                                                                                                STRAIN-C3/BL/05/14/05/14/06-10813773;
MEDLINE-20273944; PubMed=10813773;
Hirano A.A., Hack I., Waessle H., Duvoisin R.M.;
"Cloning and immunocytochemical localization of a cyclic nucleotide-
"Cloning and immunocytochemical localization of a cyclic nucleotide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cyclic-nucleotide-gated cation channel alpha 3 ((CNG-3) (CNG3) (Cyclic nucleotide gated channel in photoreceptor cGMP-gated channel alpha subunit).
                                                                                                                                                                                                                                                                                             gated channel alpha-subunit to all cone
retina.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                          MEDLINE=99307448; PubMed=10377453;
                                                                                                                                                                                       STRAIN-129/Sv;
                                                                                                                                                                                                              SEQUENCE OF 95-631 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE-Retina;
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GlnProAsnProGlyGluGlnLysProProAspGlyGlyGluGlyArgLysGluGlu---
                                                                                                                                         AlaTrpAlaSerArgHisLeuHisAspGluAspGlnThr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                  AGATGGAAGGAGACAGGTGGTGGCCGGCCCGATATGGCCGGGCACGATCCAAAGGCTTC
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                                                              AATGCCAACCGGCGGGGGGGCGGGCGTGCTCTACCACCTGTCCGGGCCACCTGCAGAAG
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TISSUE SPECIFICITY: PROMINENTLY EXPRESSED IN RETINA
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED (
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GCCATGCAC 1716	1657 GACACCACCGAGCTGCTGCAGAGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATGC	0у 1
JLYSThrVal 392	373 AspLeuGluThrArgVallleArgTrpPheAspTyrLeuTrpAlaAsnAr	Ф
Ľ	1597 CCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCACCTGGGCGGTGAACAATGGCATC	Ωу 1
WalThrLys 372	353 GluPheGlnAlaLysIleAspSerValLysGlnTyrMetGlnPheArgLysValThrLys	Дb
ATCCCCAAG 1596	1537 CTGTACCACAGCCGCACGCGCGACCTGCGCGATCCGCATCCACCGTATCCCCC	Qy 1
ProArgVal 352	333 PheAlaThrIleValGlyAsnValGlySerMetIleSerAsnMetAsnAla	DЬ
CGCCGCTTT 1536	1477 CACGCGGTGGTGTTTGGGAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCC	0у 1
TleLeuIle 332	313 ProValLysAspGluGluTyrLeuPheValValIleAspPheLeuValGl	Db
GCCCTGATG 1476	1417 GCCAACACGGACACCGAGAAGATCTTCTCCCATCTGCACCATGCTCATCGGCGCCCTGATG	Qy 1
ThrProPro 312	294 IleTyrSerLeuTyrTrpSerThrLeuThrLeuThrThrIleGlyGlu	DЬ
AACGTGTCC 1416	357 ATCACCTCCCTCTACTTCGCACTCA	Qy 1
ArgLysTyr 293	285 GluTyrAlaArgLeuSer	Db
AGCGCCTAC 1356	297 AGCGAGGCCAACGGGACGGGGCTGGAGCTGCTGGGCGGCC	Qy 1
SerLysPro 284	272GlyThrAspSerTrpValTyrProAsnThrSe	В
AACTGCAGCAGCAGC 1296	237 GTGGGCCGGAGGCCAGCTGGAGGGAACAGCTCCGGCCAGAGTGAC	Qy 1:
271	268pheIleGlyPhe	Db
TACTACCTG 1236	1177 CTGCCTGAGATTGGCTGGCTGCAGGAGCTGGCCCGACTGGAGACTCCCTACTACCTG	0у 1:
267	257 TrpAsnAlaCysIleTyrPheAlaIleSerLys	Db
GAATCCGAG 1176	1117 TGGGTCGCCTGCGTCTGGGTTTTACATTGGCCAGCGGGAGATCGAGAGCAGCGAATCCGAG	οу 1:
IleIleHis 256	237 AsnTyrProAsnValPheArgIleGlyAsnLeuValLeuTyrThrLeuIle	Db :
CTCGCGCAC 1116	1060 CAGTACAGCGCCGTGGTGCTGACACTGCTCATGGCCGTGTTCGCCCTGCTCGCGCAC	Qу 10
ThrargThr 236	217 AsnArgLeuLeuLysPheSerArgLeuPheGluPhePheAspArgThrGluT	Db .
TACTCG 1059		0у 10
LeuArgPhe 216	200 ThraspLeuAlaTyrLeuLysLeuGlyValAsnTyrProGlu	Db
CTGAAGACG 1008	949 TITGACCTGCTACATGCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACG	Qy 9
LeuIlePro 199	180 LeuTrpLysHisTyrThrLysThrLeuHisPheLysLeuAspIleLeuSerLeuIlePro	Db 1
GCCTGCCC 948		оу в
ThrLysarg 179	161 ValArgAlaArgThrGlyPheLeuGluGlnGlyLeuMetValArgAsp	
CCAAAGTCC 891		
AspMetLeu 160	141 LeuThrLeuTrpLeuValLeuAspTyrSerAlaAspValLeuTyrValLeuAspMetLeu	Db 1
SACATIGIG 831		ΩУ 7
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	LeuThrala	
TCACTGTG 726	7 CTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTAT	•
ysArgTrp 112	99ProlleValValAspProSerSerAsnIleTyrCy	•
GTGGGGCA 666	607 CCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGTGGGGCA	ОУ 6

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Q24278; Q9V7L5;
Q1-NVV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cyclic-nucleotide-gated cation channel (CNG channel).

CNG OR CG7779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-95045396; PubMed-7957070;

Baumann A., Frings S., Godde M., Seifert R.,

"Primary structure and functional expression
nucleotide-gated channel present in eyes and
EMBO J. 13:5040-5050(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S. M., Sabburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
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Pred. No.:
   Percent Similarity:
                                             Alignment Scores:
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RA Mount S.M., Woy M., Murphy B., Murphy L.M., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Relnert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Stapadling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.*,
The genome sequence of Drosophila melanogaster.*,
                                                                         CARBOHYD
CONFLICT
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InterPro; IPR000636; M+channel_nlg.
InterPro; IPR000595; cNMP_binding.
Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00520; ion_trans; 1.
SMART; SM00100; cNMP; 1.
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PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE; PS50042; CNMP_BINDING_3; 1.
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TISSUE SPECIFICITY: EXPRESSED IN ANTENNAE AND THE VISUAL SYSTEM.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
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187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            license agreement (See http://www.isb-sib.ch/announce/
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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		GCAGCAG		GCTGGCCCGCCGACTGGAGACTCCCTACTACCTGGTGGGCCGG	spSer	GGCCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGC	alleLeuvalLeuIleHisTrpAsnAlaCysMetTyrPheAlaIl	TCGCGC			ProVallleValArgLeuAsnArgLeuLeuArgIleAsnArgLeuTrpGluTrpPheAs	TGCTGC	<pre>pTrpProProGluThrCysSerSerLeuTyrLeuProCy</pre>		uArgArgHisTyrPheHisThrLysGlyTrpTyrLeuAspValLeuSerMetLeuPr	TGGT	::: :::: :::: ::: ::::	AGTCGG	- GECTIGEGACTEGGCCGTGGAGTCCTCTCATCCTTGACTTTGACATTCTGCCT 	-vaiGiyArgAlaVaiPheTrpGluIleAsnLysS	TGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCAGTGCCGCCCCCCCC	HisTyrArgTrpLeuAlaIleValSerLeuAlaValLeuTyrAsnIleIleph	TCATCC		TGCACT	::: LysIleGlyLysGlyCysProAlaMetGluAspAlaAlaLeuSerSe	3AGAAAC	 	CACCTGC	ProSerAlaLeuArgargThrLeuGlnAlaLeuArgGlnArgLeuThrLysAr		GGGGC	×	Mismate Indels .Gaps:
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nGlyTh	=	CGGGAC		AGGCCAGCTGG	Tr	TGGCTG	:::: sMetTy	CGTCTG	 sLysVa	ceccer	euTrpG1	GCTTCC	rLeuTy	CGTGTA	ll:::::	CATCGO	rgaspāl	החיבות היי	CCTTG! :: euLeuAs	leAsnLy	: 3222525	euTyrA:	ICTATG:	erValA	SAGCC-	:: spalaa	AGTACA	snThrT	AGCCCA	ACCGGC nArgLe	-SerLy	AGGAGA	65)	227 110 23
T	9	GGGGCTG		TGGAGGGAA	::: TrpvalTyrAs	GCTGCA	rPheAl	GTTTTA	lValLe	GGTGCT	uTrpPh	GCGGCT	rLeuPr	AAGGTCAACGTGTACTTCGGGGC	erMetLe	AGCGCT	laPheAr	ישבארשר ישבארשר	ACATTGI :: pThrLe	/sSerAlaPr	3CGGCCC	snIleI]	recere	spProThrLe		:::: laLeuS	AAGTAG	hrasnTl	-CAGCCCAAGGGCAAGC	GGCGGA :: uThrLy:	-SerLysArgSerLys	CAGGTG		
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                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1800
                                                                                                              Eukaryota; Metazoa;
                                                                                                                                Canis familiaris (Dog)
                                                                                                                                                  CNGA1 OR CNCG1 OR CNCG.
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 Veske A.;
             STRAIN-Beagle X Briard,
                                                                        NCBI_TaxID=9615;
                                                                                           Mammalia; Eutheria; Carnivora;
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uProAspLysLeuLysAlaGluIleAlaIleGlnValHisMetAspThrLeuLysGlnVa
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                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                             Fissipedia; Canidae; Canis
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GACATCAGCGAAACCAAGAACCGAGGGGGCCCCCGACAGATGGAAGGAGACAGGTGGTGGC 453

ProSerGlnArgGluGlnTyrLeuProGlyAlaIleAlaLeuPheAsnValAsnAsnSer

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                                                                                                                          Query Match:
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00888; CNMP_BINDING_1; PROSITE; PS00889; CNMP_BINDING_2; PROSITE; PS50042; CNMP_BINDING_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00520; ion_trans; SMART; SM00100; CNMP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
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FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMOTETRAMER OR HIGHER OLIGOMER. SUBCELLULAR LOCATION: Integral membrane p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS
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     CCCATAAAGAATGAGAAA----
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IPR000595; cNMP_binding.
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CYTOPLASMIC (POTENTIAL)
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•	CTG 1329	1270 GGCCAGAGTGACAACTGCAGCAGCAGCGAGGCCAACGGGACGGGGCTGGAGCTGCTG	Ş
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	::: Val 209	192 GlnSerAspTyrLeuGluTyrTrpIleIlePheAspTyrLeuSerAspIleVal	В
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MEDLINE-92210603; PubMed-1372902;
Baehr W., Wasmuth J.J., Hurwitz R.L.,
Altherr M.R., Lee A.K., Pittler S.J.;
"Primary structure and chromosomal loc
                                                                                                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; 
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                                                          TISSUE-Retina;
                                                                       SEQUENCE FROM N.A.
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Rodentia;
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Sciurognathi; Muridae;
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human and mouse
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SOLUTION OF THE TEST STATES OF THE STATES OF
                                                           Alignment Scores:
Percent Similarity:
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Biophim. Biophys. acta 123s:197-200(1995).

-I- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN CAN.
COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN.
BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by an entities required a lighter to the statement is not removed.
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Stanton B.A.;
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InterPro; IPR000595; cNMP_binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
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·--ProLysAspLeuGluGluLysValThr
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US-09-965-830-1_COPY_6_3257 (1-3252) x CNG_ICTPU (1-682)

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Percent Similarity:
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Query Match:
DB:
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CNG_ICTPU
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InterPro; IPR000636; M+channel_nlg.
InterPro; IPR001201; PAP_25A_core.
InterPro; IPR000595; cNMP_binding.
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                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00027; cNMP_binding; Pfam; PF00520; ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no use by non-profit institutions as long as its conmodified and this statement is not removed. Usage b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning and single-channel nucleotide-gated channel from catfish Neuron 8:45-58(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ictalurus punctatus (Channel catfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Ictaluridae; Ictalurus.
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01-NOV-1997
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P55934;
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-I- TISSUE SPECIFICITY: OLFACTORY NEURONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Olfactory neuroepithelium;
MEDLINE-92110008; PubMed-1370374;
                                                                                                                                                                                                                                                                                               Conic
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                          CAMP
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                                                                                                                                                                    H5 (POTENTIAL)
                                                                                                                                                                              H4 (POTENTIAL)
CYTOPLASMIC (F
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H1 (POTENTIAL).
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                                                                                                                                                                                                                                                                                         cAMP-binding; Transmembrane;
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Conservative: Mismatches: Indels: Gaps:
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Matches:
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306	304TrpWalTyr	Db
TG 1236	99	Qy
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AG 1176	TGGGTCGCCTGCGTCTTTTACATTGGCCAGCGGGAGATCGAGAGCAGCGAATCCC	O 5
AC 1116	1060 CAGTACAGCGCCCTGGTGCTCGACACTGCTCATGGCCCTGTTTCGCCCCTGCTCGCGCACACTGCTATGGCCCTGTTTCGCCCCTGCTCGCGCACACTGCTATGGCCCGTGTTCGCCCTGCTCGCGCGACACTGCTGCTATGGCCGTGTTCGCCCTGGTGCTGACACTGGCCGTGTTCGCCACACTGCACACTACACTACACACTACACACTACACACTAC	P 24
N		ДĎ
CG 1059		VΩ
ĕ	29 ThrGluLeuLeuPhePheValThrGlyTyrValProGlnLeuArg	B. 5
10	GGCCCATCTGCTGAAGA	9 5
CC 948 7	92 ATTTGCCTCCACTACGTCACCACCTGGTTCCTGCTGGATCTCATCGAGCGCTCC :::: ::: ::: ::: ::: ::: ::::	P 09
20	rLeuGluGlnGlyLeuLeuValLysAs	ф
00	TTTCCGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTGTTTTGC	Qy
ys 189	174 ValGlyLeuAspTyrLeuCysAspValIleTyrlieLeuAspThrCy	밁
TG 831	775GGCCGCCCAGCGTCTGTGACCTGGCCGTGGAGGTCCTCTTCATCCTTGACATTGTG	Qy
rp 173	154 IleMetLeuValAlaArgAlaCysPheAspGlnLeuGlnAspGluAsnPhePheLeuTr	Db
774	TCACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGGGGAGCCCAGTGCCGCCCGC	Qy
rp 153	134 SerAspAspIleTyrTyrTyrTrpLeuPhePheIleAlaLeuAlaSerLeuTyrAsnTr	В
OT 717	G	Qy
ln 133	LysThrPheLysGluArgTrpGluGlyPheValValSerGl	망
AC 657	TIGO	Qy
113	113	뮹
VA 597	538 CACCTGCAGAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGGTGTTTGGGGAGAAA	Qy
113	101 PheArgGlyProGlnAlaAlaAsnAspGlnSerAlaAla	Db
3G 537	GGCTTCAATGCCAACCGGCGCG	Qy
g 100	94ProAspSerPheLeuGluArg	망
A 477	AGATGGAAGG	Qy
.g 93	74 AsnLeuValLeuSerLeuArgGluTrpAlaHisLysSerLeuValGluThrGluGlnArg	ф
;A 417	373 CTCTTCCTAGTCTCT	Qy
1 73	54 LeuProSerAlaGluMetLeuGluAlaPheThrGlnArgArgProLeuAlaArgLeuVal	Дb
T 372	313 CTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAAGGGGGAGGTGGCT	Qy
ւս 53	 34 SerArgThrAspGlyAspAspAspThrCysSerGluLeuGlnArgValThrAlaLeuGlu	멍
- 312	298 TACCGGAAGAGCGGG	Qy
e 33	::: ::: ::: ::: :::	문
G 297	CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTT	Qy

GTC 2223	2164 AATACCCTTATGTCCACGCTGGAGGAGGAGGAGGACAGATGGGGGAGCAGGGCCCCACGG	Qy	
Cys 635	$616\ {\tt PheThrSerThrGlnArgArgLeuLysGlnArgIleThrAlaLeuGluArgGlnLeuC}$	Db	
2163	2163	Qy	
Glu 615	596 GluArgLeuAspAlaSerLeuAspIleLeuGlnThrArgPheAlaArgLeuLeuGlyGlu	Db	
	2146AGCTCCCTGAGCGGCGAC	Qy	
Val 595	576 LeuLeuAspGluSerValAlaAlaGlyGlyLeuGlyValIleAspThrGluGluLysV	Db	
2145	2116GCTGGGGGAGGCTCTGCAGAGGTGGACACC	Qy	
31y 575	557 ProAspAlaGlnLysValLeuGluGluArgGlyArgGluIleLeuArgLysGlnGly	Db	
3GT 2115	AACC	Qy	
Tyr 556		망	
FAC 2055	- ფ	Qy	
::: [le 536		B .	
TG 1995	1939TGTGAGCTGCCCCGGCGGAGCAGGTGGTAAAGGCCCAATGCCGACGTGAAGGGGCTG	Qy	
3er 516	497 AspAspGlyValThrGlnPheAlaLeuLeuThrAlaGlyGlyCysPheGlyGluIleSer	망	
1938	1891AAGGGTGGCACCGTGCTCGCCATCCTAGGGAAGGGCGACCTGATCGGC	Qy	
1la 496	477 LysGlyAspIleGlyLysGluMetTyrIleIleLysGluGlyGlnLeuAlaValNalAla	Дb	
1890	1834 CAAGGCGATGCCCTGCAGGCCCCTCTACTTTGTCTGCTCTGGCTCCATGGAGGTGCTC-	Qy	
rg 476	457 ValGluLeuValLeuLysLeuArgProGlnValTyrSerProGlyAspTyrIleCysArg	Db	
AC 1833	1774 CGGGCACTGTCTCTGGCCCTGCGGCCCTTCTGCACGCCGGGCGAGTACCTCATCC	Qy	
eu 456	437 ValHisLeuAspThrLeuLysLysValArgIlePheGlnAspCysGluAlaGlyLeuLeu	Db	
TG 1773	1717 CTGCACAAGGAGGTCCTGCAGCTGCCACTGTTTGAGGCGGCCAGCCGGGGTGCC	Qy	
sn 436	417 AspGluGlnGluValLeuLysAsnLeuProAspLysLeuArgAlaGluIleAlaIleAsn	Db	
AC 1716	1657 GACACCACCAGCTGCTGCAGAGCCTCCCTGACGAGCTGCGCCGAGACATCGCCATGCI	Qy	
al 416	397 ThrLeuGluThrArgVallleLysTrpPheAspTyrLeuTrpThrAsnLysLysThrVal	В	
TC 1656	1597 CCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCACCTGGGCGGTGAACAATGGCAT	Qγ	
rg 396	377 GlupheGlnThrArgIleAspAlaIleLysHisTyrMetHisPheArgLysValAsnArg	망	
AG 1596	1537 CTGTACCACAGCGGGACGGGGACCTGCGGGACTACATCCGCATCCACGGTATCCCCAAG	Qy	
la 376	357 PheAlaThrIleValGlyAsnValGlySerMetIleAlaAsnMetAsnAlaThrArgAl	Дb	
TT 1536	1477 CACGCGGTGGTGTTTGGGAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCC	Qy	
le 356	338 ValLysAspGluGluTyrValPheValValPheAspPheLeuValGlyValLeuIle	Db	
TG 1476	1417 GCCAACACGGACACCGAGAAGATCTTCTCCATCTGCACCATGCTCATCGGCGCCCCTGAT	. Qy]	
ro 337	318 ValTyrCysPheTyrTrpSerThrLeuThrLeuThrThrIleGlyGluMetProProPro	Db	
CC 1416	357	Qy 1	
yr 317	311LysThrLeuSerPheCysTy	Db	
AC 1356	1297 AGCGAGGCCAACGGGACGGGGCTGGAGCTGCTGGGGGGGCCCGTCGCTGCGCAGCGCCTAC	Qy	
310	307	Db	
3C 1296	1237 GTGGGCCGGAGGCCAGCTGGAGGGAACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGC	Qy 1	

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                                                                                                                                            photoreceptors.";
J. Biol. Chem. 267:644-648(1992).
-I. FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN FUNCTION: VISUAL SIGNAL SECOND MESSENGER. THIS PROTEIN CAPPEDED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAPPEDED CASCADE USING MAICH LEADS TO A ODENING OF THE CATIC BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A ODENING OF THE CATIC BE ACTIVATED BY CAUSING A DEPOLARIZATION OF ROD
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                                                                                                                     <del>:</del>
                                                                                                                                                                                                                                                                                                         MEDLINE=95365381; PubMed=7543681; Henn D.K., Baumann A., Kaupp U.B.; "Probing the transmembrane topology of cyclic nucleotide-gated channels with a gene fusion approach."; Proc. Natl. Acad. Sci. U.S.A. 92:7425-7429(1995).
                                                                                                                                                                                                                                    MEDLINE=92112723; PubMed=1370452; Wohlfart P., Haase W., Molday R.S., Cook N.J.; Wantibodies against synthetic peptides used to deterand site of glycosylation of the CGMP-gated channel
                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular model of the cyclic GMP-binding gated ion channel."; Biochemistry 31:4643-4649(1992).
                                                                                                                                                                                                                                                                                               TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                         3D-STRUCTURE MODELING OF 485-610.
MEDLINE-92256398; PubMed=1316156;
Kumar V.D., Weber I.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Primary structure and functional expression from oc
of the rod photoreceptor cyclic GMP-gated channel.",
Nature 342:762-766(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG-1)
(Cyclic nucleotide gated channel alpha 1) (Cyclic nucleotide gated channel, photoreceptor) (Cyclic-nucleotide-gated channel, photoreceptor) (Cyclic-nucleotide-gated channel)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stuehmer W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOVIN
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01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaupp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90098076; PubMed=2481236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FISSUE-Retinal rod cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNG1_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2224 TCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
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mer W., Cook N.J.,
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O THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
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                                                                                                                                                                                                                                                                                                                                                                                                        52 SerGluThrGluAsnProHisAlaArgAspSerPheArgSerAsnThrHisGlySerGly
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1293	CTGGTGGGCCGGAGGCAGCTGGAGGGAACAGCTCCGGCCAGAGTGACAACTGCAGCAGC	Qy
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p29973; Q16485; Q16279;
01-APR-1993 (Rel. 25, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
CGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG-1)
CCYClic nucleotide gated channel alpha 1) (Cyclic nucleotide gated channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)
(Rod photoreceptor CGMP-gated channel alpha subunit).
CNGA1 OR CNCG1 OR CNCG.
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"Primary structure and chromosomal localization of human and mouse rod photoreceptor cGMP-gated cation channel.";
J. Biol. Chem. 267:6257-6262(1992).
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                                                                                                                                                                                                                                                                                                                                                     "Human rod photoreceptor cGMP-gated channel: amino acid sequence, gene structure, and functional expression.";
J. Neurosci. 12:3248-3256(1992).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        613 AsnAlaGlySerAsp------ProLysAspLeuGluGluLysValThr 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yau K.-W., Nathans J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dhallan R.S., Macke J.P., Eddy R.L., Shows T.B., Reed R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
VARIANT ARRP PHE-316, AND VARIANTS GLN-28 AND ASN-114
MEDLINE=96036047; PubMed=7479749;
                                                                                                  Neuropharmacology 33:1275-1282(1994).
                                                                                                                                                                                                               Distler M.,
                                                                                                                                                                                                                                        SEQUENCE OF 313-573 FROM N.A. MEDLINE-95175019; PubMed-7532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92356211; PubMed=1379636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92210603; PubMed-1372902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                         sion of cyclic nucleotide-gated cation channels and cells.";
                                                                                                                                                                                                            75019; PubMed=7532814;
Biel M., Flockerzi V.,
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                                                                                                                                                                                                                          Hofmann F.;
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InterPro; IPR000595; cNMP_binding.
Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00520; ion_trans; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; S42457;
EMBL; S76062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mutations in the gene encoding the alpha subunit of the rod cGMP-gated channel in autosomal recessive retinitis pigmentosa."; Proc. Natl. Acad. Sci. U.S.A. 92:10177-10181(1995).

-i- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A42161; A42161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    onic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SÜBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: ROD CELLS IN THE RETINA.
DISEASE: DEFECTS IN CNGAL REA CAUSE OF AUTOSOMAL RECESSIVE
RETINITIS PICMENTOSA (ARRP). A DISEASE THAT LEADS TO DEGENERATION
OF RETINAL PHOTORECEPTOR CELLS.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATTON CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATABASE: NAME-Mutations of the CNGAl gene; NOTE-Retina International's Scientific Newsletter; WWW-"http://www.retina-international.com/sci-news/cngalmut.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMOTETRAMER OR HIGHER OLIGOMER. FORMS HETEROOLIGOMERIC
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AAB22778.1; -.
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Disease mutation;
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Polymorphism;
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{\tt LeuArgPheSerArgMetPheGluPhePheGlnArgThrGluThrArgThrAsnTyrProperty} \\
                                  GTGCGCCTGCTGCGCCTGCCTGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGC
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US-09-965-830-1_COPY_6_3257 (1-3252) x CNG1_HUMAN (1-686)
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SEQUENCE
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AspLeuLeuTyr---PheLysLeuGlyTrpAsnTyrProGluIleArgLeuAsnArgLeu
                                          GACCTGCTACATGCCTTCAAGGTCAAC---GTGTACTTCGGGGCCCATCTGCTGAAGACG
                                                                                IleAsnLysTyrLysSerAsnLeuGlnPheLysLeuAspValLeuSerLeuIleProThr
                                                                                                                        ATTTGCCTCCACTACGTCACCACCTGGTTCCTGCTGGATGTCATCGCAGCGCTGCCCTTT
                                                                                                                                                                   ValArgThrArgThrGlyTyrLeuGluGlnGlyLeuLeuValLysGluGluLeuLysLeu
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                                                                                                            AAGGGGCTGACGTACTGCGTCCTGCAGTGTCTGCAGCTGGCCTGCACGACAGCCTT
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                                                                       LysSerIleGlyTyrSerAspLeuPheCysLeuSerLysAspAspLeuMetGluAlaLeu
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RESULT 14
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-NOV-1997 (Rel.
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InterPro; IPR000595; cNMP_binding.
Pfam; PF00027; cNMP_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molday R.S., Kaupp U.B.;
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                                         TRANSMEM
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PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE; PS50042; CNMP_BINDING_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATIC CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GGGGAGCTCAGCTACAACCTGGGTGCTGGGGGGAGGCTCTGCAGAGGTGGACACCAGC 2148
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Last annotation update)
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CAMP (BY SIMILARITY)
CAMP (POTENTIAL).
                                                                   EXTRACELLULAR H6 (POTENTIAL)
                                                                                                                                                             H4 (POTENTIAL)
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                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
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Query Match:
DB:
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                       CTCAGCAGCCTCACCAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGGACACCGAGAAG
                                                            GlyAlaAspThrTrpValTyrProAsnThrSerHisProGluPheAlaArg------
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                           SEQUENCE FROM N.A. TISSUE-Aorta;
                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                     01-NOY-1997 (Rel. 35, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated cation channel 2) (CNG channel 2) (CNG-2) (CNG-2) (Aorta CNG channel
                                                                                                                                  CNGA2 OR CNCG2
                                                                                                                                                                                                                                         CNG2_RABIT Q28718;
                                                                        NCBI_TaxID=9986
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                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Lagomorpha; Leporidae; Oryctolagus.
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MEDLINE=93359035; PubMed=7689061; Biel M., Altenhofen W., Hullin R.

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FEBS Lett. 329:134-138(1993).
-!- FUNCTION: ODORANT SIGNAL TRANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.ish-
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                                                                                                                                                                                                                                                                                                                                     BINDING
CARBOHYD
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InterPro; IPR000636; M+channel_nlg.
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52 ArgLeuAlaGluMetAspAlaProGlnGlnArgArgGlyGlyPheArgArgIleValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
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                                                       Ser \texttt{ArgThrArgSerArgProGlnSerAlaAlaAspAspAspThrSerSerGluLeuGln}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00888; CNMP_BINDING_1;
PS00889; CNMP_BINDING_2;
PS50042; CNMP_BINDING_3;
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174
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38.84%
23.95%
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     648 TyrLeuSerAspGlyMetAsnSerPro--
                                                                                              628 LysLeuLysGlnArgIleThrValLeuGluValLysMetLysGlnAsnThrGluAspAsp 647
                                                                                                                                                                                                608 MetGluThrLeuTyrThrArgPheGlyArgLeuLeuAlaGluTyrThrGlyAlaGlnGln 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1852 GCCCTCTACTTTGTCTGCTCTGGCTCCATGGAGGTGCTC-----AAGGGTGGCACCGTG 1905
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                                                                                                                                                                                                                                                                                                                                                                                                      570 LeuGluGluArgGlyArgGluIleLeuMetLySGluGlyLeuLeuAspGluAsnGluVal 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 TyrAlaLeuLeuSerAlaGlySerCysPheGlyGluIleSerIleLeuAsnIleLysGly 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490 GluMetTyrileIleLysGluGlyLysLeuAlaValValAlaAspAspGlyValThrGln 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1495 AACGTGACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTACCACAGCCGCACG 1554
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                                                                                                                                                                                                                                                                        ATGTCCACGCTG----
-GluProAlaAlaAlaGluGlnPro 664
                                                                                                                                                  ---GAGGAG 2190
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